

**AMENDMENTS TO THE CLAIMS**

Claim 26 (Currently amended): A method of screening for neoplastic cells in a sample, the method comprising:

contacting a nucleic acid sample from a human patient with a ~~probe consisting~~ probe consisting essentially of a sequence of SEQ. ID. No. 9, wherein the probe is contacted with the sample under conditions in which the probe specifically hybridizes under stringent conditions with the ~~target polynucleotide sequence~~ nucleic acid sample to form a stable hybridization complex; and

detecting the formation of a hybridization complex, wherein an amplification of said target polynucleotide sequence indicates that said cell is a neoplastic cell.

Claim 27 (Previously presented): The method of claim 26, wherein the nucleic acid sample is from a patient with breast cancer.

Claim 28 (Previously presented):. The method of claim 26, wherein the nucleic acid sample is a metaphase spread or an interphase nucleus.

Claim 48 (Previously presented): A method of screening for neoplastic cells in a sample, the method comprising:

contacting a nucleic acid sample from a human patient with a probe that hybridizes selectively to a target polynucleotide sequence consisting essentially of the sequence of SEQ. ID. No. 10, wherein the probe is contacted with the sample under conditions in which the probe specifically hybridizes under stringent conditions with the target polynucleotide sequence to form a stable hybridization complex; and

detecting the formation of a hybridization complex, wherein an amplification of said target polynucleotide sequence indicates that said cell is a neoplastic cell.

Claim 49 (Previously presented): The method of claim 47, wherein the nucleic acid sample is from a patient with breast cancer.

Claim 50 (Previously presented): The method of claim 47, wherein the nucleic acid sample is a metaphase spread or an interphase nucleus.

Claim 51 (Currently amended):      The method of claim 47, wherein the probe ~~comprises~~ consists of  
a polynucleotide sequence as set forth in SEQ. ID. No. 10.